

1644

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/060,872

DATE: 07/24/2000
TIME: 17:01:07

Input Set : A:\GC527D2.APP.txt
Output Set : N:\CRF3\07242000\I060872.raw

ENTERED

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JUL - 7 2001

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#20 SK 8/8/00

3 <110> APPLICANT: Estell, David
4 Harding, Fiona
6 <120> TITLE OF INVENTION: Mutant Proteins Having Lower Allergenic Responses in
7 Humans and Methods for Constructing, Identifying and
8 Producing Such Proteins
10 <130> FILE REFERENCE: GC 527-D2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/060,872
C--> 13 <141> CURRENT FILING DATE: 1998-04-15
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1494
21 <212> TYPE: DNA
22 <213> ORGANISM: Bacillus amyloliquefaciens
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25 <221> NAME/KEY: CDS
26 <222> LOCATION: (96)..(1244)
28 <220> FEATURE:
29 <221> NAME/KEY: mat_peptide
30 <222> LOCATION: (417)..(1241)
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35 ttattctgca aatgaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta 113
36 Val Arg Gly Lys Lys Val
37 -105
39 tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161
40 Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
41 -100 -95 -90
43 ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209
44 Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
45 -85 -80 -75 -70
47 aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257
48 Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
49 -65 -60 -55
51 aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa 305
52 Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
53 -50 -45 -40
55 ttc aaa tat gta gac gca gct tca gct aca tta aac gaa aaa gct gta 353
56 Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr Leu Asn Glu Lys Ala Val
57 -35 -30 -25
59 aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac 401
60 Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His
61 -20 -15 -10
63 gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att 449
64 Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile
65 -5 -1 1 5 10
67 aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa 497

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68 Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
69      15      20      25
71 gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag 545
72 Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys
73      30      35      40
75 gta gca ggc gga gcc agc atg gtt cct tct gaa aca aat cct ttc caa 593
76 Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln
77      45      50      55
79 gac aac aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt 641
80 Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu
81 60      65      70      75
83 aat aac tca atc ggt gta tta ggc gtt gcg cca agc gca tca ctt tac 689
84 Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr
85      80      85      90
87 gct gta aaa gtt ctc ggt gct gac ggt tcc ggc caa tac agc tgg atc 737
88 Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile
89      95      100      105
91 att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac 785
92 Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn
93      110      115      120
95 atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt 833
96 Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val
97      125      130      135
99 gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac 881
100 Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Ala Gly Asn
101 140      145      150      155
103 gaa ggc act tcc ggc agc tca agc aca gtg ggc tac cct ggt aaa tac 929
104 Glu Gly Thr Ser Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr
105      160      165      170
107 cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca 977
108 Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala
109      175      180      185
111 tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta 1025
112 Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val
113      190      195      200
115 tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt 1073
116 Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly
117      205      210      215
119 acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt 1121
120 Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
121 220      225      230      235
123 tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta gaa 1169
124 Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu
125      240      245      250
127 aac acc act aca aaa ctt ggt gat tct ttc tac tat gga aaa ggg ctg 1217
128 Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu
129      255      260      265
131 atc aac gta cag gcg gca gct cag taa aacataaaaa accggccttg 1264
132 Ile Asn Val Gln Ala Ala Ala Gln

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135 gccccgcgcg ttttttattt ttcttctctc gcatgttcaa tccgctccat aatcgacgga 1324
137 tggtccctc tgaaaatttt aacgagaaac ggcgggttga cccggtcag tcccgtaacg 1384
139 gccaaagtctt gaaacgtctc aatcgccgct tcccggtttc cggtcagctc aatgccgtaa 1444
141 cggtcggcgcg cgttttctcg ataccgggag acggcattcg taatcggatc 1494
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 382
146 <212> TYPE: PRT
147 <213> ORGANISM: Bacillus amyloliquefaciens
149 <400> SEQUENCE: 2
150 Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
151 1 5 10 15
153 Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly
154 20 25 30
156 Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met
157 35 40 45
159 Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
160 50 55 60
162 Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
163 65 70 75 80
165 Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
166 85 90 95
168 Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro
169 100 105 110
171 Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr
172 115 120 125
174 Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser
175 130 135 140
177 Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala Ser Met Val Pro Ser
178 145 150 155 160
180 Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His Gly Thr His Val Ala
181 165 170 175
183 Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala
184 180 185 190
186 Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser
187 195 200 205
189 Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn
190 210 215 220
192 Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala
193 225 230 235 240
195 Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val Val
196 245 250 255
198 Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser Thr Val
199 260 265 270
201 Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly Ala Val Asp
202 275 280 285
204 Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly Pro Glu Leu Asp
205 290 295 300
207 Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys

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208 305          310          315          320
210 Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly
211          325          330          335
213 Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp Thr Asn Thr Gln
214          340          345          350
216 Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe
217          355          360          365
219 Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
220          370          375          380
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 275
225 <212> TYPE: PRT
226 <213> ORGANISM: Bacillus subtilis
228 <400> SEQUENCE: 3
229 Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu
230 1          5          10          15
232 His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
233          20          25          30
235 Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly Gly Ala
236          35          40          45
238 Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
239          50          55          60
241 Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
242 65          70          75          80
244 Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
245          85          90          95
247 Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
248          100          105          110
250 Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
251          115          120          125
253 Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
254          130          135          140
256 Ser Gly Ile Val Val Ala Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
257 145          150          155          160
259 Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
260          165          170          175
262 Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
263          180          185          190
265 Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
266          195          200          205
268 Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
269          210          215          220
271 Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
272 225          230          235          240
274 Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
275          245          250          255
277 Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
278          260          265          270
280 Ala Ala Gln

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281          275
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 274
286 <212> TYPE: PRT
287 <213> ORGANISM: Bacillus licheniformis
289 <400> SEQUENCE: 4
290 Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
291      1          5          10          15
293 Gln Ala Gln Gly Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp
294          20          25          30
296 Thr Gly Ile Gln Ala Ser His Pro Asp Leu Asn Val Val Gly Gly Ala
297          35          40          45
299 Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly
300          50          55          60
302 Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
303          65          70          75          80
305 Leu Gly Val Ala Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn
306          85          90          95
308 Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile Val Ser Gly Ile Glu Trp
309          100         105         110
311 Ala Thr Thr Asn Gly Met Asp Val Ile Asn Met Ser Leu Gly Gly Ala
312          115         120         125
314 Ser Gly Ser Thr Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg
315          130         135         140
317 Gly Val Val Val Val Ala Ala Ala Gly Asn Ser Gly Asn Ser Gly Ser
318          145         150         155         160
320 Thr Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
321          165         170         175
323 Gly Ala Val Asp Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly
324          180         185         190
326 Ala Glu Leu Glu Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr
327          195         200         205
329 Pro Thr Asn Thr Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro
330          210         215         220
332 His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu
333          225         230         235         240
335 Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu
336          245         250         255
338 Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
339          260         265         270
341 Ala Gln
345 <210> SEQ ID NO: 5
346 <211> LENGTH: 269
347 <212> TYPE: PRT
348 <213> ORGANISM: Bacillus lentus
350 <400> SEQUENCE: 5
351 Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
352      1          5          10          15
354 His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/060,872

DATE: 07/24/2000

TIME: 17:01:08

Input Set : A:\GC527D2.APP.txt

Output Set: N:\CRF3\07242000\I060872.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date